This listing of claims will replace all prior versions, and listings, of claims in the application.

## Listing of Claims:

1. (currently amended) A method of using a mutation scanning array, wherein said mutation scanning array comprises a plurality of elements, wherein the elements contain immobilized oligonucleotides 8 - 50 bases long, that collectively span at least 10 different array genes from the 5' to 3' end, wherein the array genes can be either coding regions or ~~the~~ genomic genes, to identify whether a target DNA contains any genes which are present on the array and contain mutations, ~~mutations in a target DNA sequence~~ which comprises:

(a) hybridizing the target DNA with a control DNA sequence to create a duplex, wherein the control DNA sequence is the wild-type DNA corresponding to the target DNA sequence~~, and wherein said target DNA comprises a pool of nucleotide segments that collectively span at least 10 different genes~~,

(b) tagging any mismatch in said duplex with a detectable moiety,

(c) cleaving the duplex into segments of 50 - 300 bases,

(d) removing the segments tagged with the detectable moiety,

(e) contacting the segments tagged with the detectable moiety with the mutation scanning array, and

(f) identifying in which array gene and gene segment thereof the selected mismatch belongs to, wherein at least ten different array genes are examined at the same time.

2. (previously amended) The method of claim 1, wherein the segments tagged with the detectable moiety are amplified before being used on the mutation scanning array.

3. (currently amended) The method of claim 1 or 2, wherein each ~~the~~ whole gene on the mutation scanning array is represented by array elements; each element containing immobilized oligonucleotides that sample in 25-300 bases for the whole 3' to 5' mRNA sequence of each represented gene.

4. (currently amended) The method of claim 1 or 2, wherein each of the array genes is represented by the coding portion of the gene.

5. (currently amended) The method of claim 1 or 2, wherein each of the array genes is represented by both the coding and non-coding genomic portions of a gene.

6. (currently amended) The method of claim 1 or 2, wherein said at least 10 different array genes are collectively known to predispose an individual to a particular disease.

7. (original) The method of claim 6, where the disease is a particular kind of cancer.

8. (original) The method of claim 6, where the disease is a cardiovascular abnormality, or a neurodegenerative disorder, or diabetes.

9. (currently amended) The method of claim 1 or 2, where said array genes are all known tumor suppressor genes or oncogenes.

10. (currently amended) The method of claim 1 or 2, where said array genes are genes known to be overexpressed in a malignant cell, wherein overexpression is determined by comparison to the gene's expression in a corresponding non-malignant cell.

11. (original) The method of claim 1, wherein the array is a chip or a microsphere.

12. (previously amended) A method of using a mutation scanning array to identify mutation in a target DNA sequence, wherein said mutation scanning array comprises a plurality of

elements, wherein the elements contain immobilized oligonucleotides 8 - 50 bases long, that collectively span at least 5 different genes, wherein said method comprises:

(a) hybridizing the target DNA sequence with a control DNA sequence wherein said control DNA sequence is the wild-type DNA sequence corresponding to the target DNA sequence to create a duplex, and wherein said target DNA comprises a pool of nucleotide segments that collectively span at least 5 different genes;

(b) digesting the duplex to fragments of 50-300 base pairs, with restriction enzymes that allow generic addition of PCR primers;

(c) adding PCR primers to the duplex

(d) treating the duplex to remove any spontaneous aldehydes;

(e) reacting the duplex with a repair glycosylase to convert any mismatched sites in the duplex to reactive sites containing an aldehyde-containing abasic site;

(f) reacting the duplex with a compound of the formula X-Z-Y, wherein X is a detectable moiety, Y is NHNH2, O-NH2 or NH2, and Z is a hydrocarbon, alkyhydroxy, alkylethoxy, alkylester, alkylether, alkylamide or alkylamine, wherein Z may be substituted or unsubstituted; or where Z may contain a cleavable group; for a sufficient time and under conditions to covalently bind to the reactive sites;

(g) detecting the bound compound to identify sites of mismatches;

(h) isolating the DNA that contains mismatches from DNA without mismatches;

(i) PCR-amplifying the mismatch-containing DNA

(j) applying the mismatch-containing DNA on the Mutation Scanning Array, to determine the genomic position(s) where mismatches occur; and

k) determining whether the mismatch is a mutation or polymorphism.

13. (original) The method of claim 12, where the detectable moiety is selected from the group consisting of $NH_2$, SH, $NHNH_2$, a fluorescein derivative, a hydroxycoumarin derivative, a rhodamine derivative, a BODIPY derivative, a digoxigenin derivative and a biotin derivative.

14. (withdrawn) A method of using a mutation scanning array to identify a common mutation in a group of at least 5 individuals having a disease comprising:

a) obtaining DNA or mRNA from said group of individuals;

b) digesting the DNA or mRNA into fragments of 50-200 base pairs;

c) identifying and tagging those fragments, creating tagged fragments, where a mismatch is present when said fragment is compared with a control wild-type fragment; and specifically labelling DNA or mRNA from each member of the group;

d) isolating said tagged fragments;

e) PCR-amplifying said tagged fragments using primers labeled with a probe, creating labeled DNA;

f) mixing the labeled DNA with a microsphere, wherein said microsphere contains single strand DNA of 50-300 base pairs obtained from wild-type genes of interest, under conditions permitting hybridization under moderate stringency;

g) subjecting the hybridized microsphere of step (f) to flow cytometry to sort in the same container those microbeads containing identical signals for a mutation from at least two members of said group; and

h) identifying in which gene and gene segment the common mutation occurs.

15. (withdrawn) The method of claim 14, wherein the flow cytometry is used to select identical signals from at least 50% of said group of individuals.

16. (currently amended) The method of claim 12, wherein the target DNA sequence comprises at least 5 ~~contiguous~~ genes, each of which is contiguous.

17. (new) The method of claim 12, wherein the segments tagged with the detectable moiety are amplified before being used on the mutation scanning array.

18. (new) The method of claim 12, wherein each whole gene on the mutation scanning array is represented by array elements; each element containing immobilized oligonucleotides that sample in 25-300 bases for the whole 3' to 5' mRNA sequence of each represented gene.

19. (new) The method of claim 12, wherein each of the array genes is represented by the coding portion of the gene.

20. (new) The method of claim 12, wherein each of the array genes is represented by both the coding and non-coding genomic portions of a gene.

21. (new) The method of claim 12, wherein said at least 10 different array genes are collectively known to predispose an individual to a particular disease.

22. (new) The method of claim 21, where the disease is a particular kind of cancer.

23. (new) The method of claim 21, where the disease is a cardiovascular abnormality, or a neurodegenerative disorder, or diabetes.

24. (new) The method of claim 22, where said array genes are all known tumor suppressor genes or oncogenes.

25. (new) The method of claim 12, where said array genes are genes known to be overexpressed in a malignant cell, wherein overexpression is determined by comparison to the gene's expression in a corresponding non-malignant cell.